Preparation for Term Paper
(Genetic Mapping Methods/Articles)

Previous Experience with Genetic Map Files

- In [this blog post](#), I discuss decent broad ancestry chromosome painting with human data but unsatisfactory *RFMix* analysis with cat data.

- So, I went back to check more information about how those genetic mapping files were created.

SHAPEIT Method

- There is a *Biostars* discussion related to genetic map creation here.
- For **human data**, I believe the recommendation is to use *HapMap* data (such as here and here, with a reference to the Delaneau et al. 2014 citation).
- For the **cat data**, my notes indicate that some data was uploaded here and there was a *create_genetic_map_files_from_Li_et_al_2016-felCat8.pl* script that was run **prior** to running *SHAPEIT*.
  - The Li et al. 2016 publication provides cM distances in the supplemental material.
  - *CRI-MAP* was used for linkage analysis (with use of *two-point*, *autogroup*, *build* and *flips* options).
    - I can find some currently hosting of code here, with a tutorial here.
- On the GitHub Page, it looks like the citation for *SHAPEIT5* is Hofmeister et al. 2023.

Literature Search for Articles Related to Genetic Map Creation

- Markelz et al. 2017 has a section titled "*Genetic map construction*", which mentions using R/QTL and a *ripple()* function.

- Hall et al. 2001 is described as software for "*Creating Integrated Physical and Genetic Maps*".
    - The introduction mentions *SEGMAP* (Green and Green 1991) for STS markers.

- Coe et al. 2002 describe a physical and genetic map for maize, including a reference to Davis et al. 1999 with the use of *MAPMAKER*.

- Baird et al. 2008 describe the use of genetic mapping with **RAD (Restriction-site Associated DNA)** Markers through a **sequencing-based strategy** (with >3,000 citations).

- Sim et al. 2012 describe creating a tomato genetic map with SNP-chip data, with the use of *JoinMap 4.0* (where I believe ***JoinMap 5.0*** is currently available), *Map Manager QTXb20* (Manly et al. 2001 has >1,000 citations - now available on GitHub?), and *MapChart* software (Voorrips 2002 - >5,000 citations).

- Libiger et al 2009 compare genetic distance measures (in humans), which is cited by Bansal et al. 2010.

- Cheema and Dicks 2009 provide a review of methods available for genetic mapping in plants (at least at the time of publication).

- Meng et al. 2015 describe the *QTL IciMapping* method, for use with biparental populations.

- Rajurkar et al 2019 describe using *Map Manager QTX* with the *Haldane* mapping function.